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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/895,435	06/30/2001	A. Francis Stewart	9882-012	8975

7590 09/22/2004

Craig J. Arnold, Esq.
AMSTER, ROTHSTEIN & EBENSTEIN LLP
90 Park Avenue
New York, NY 10016

EXAMINER	
MCGARRY, SEAN	
ART UNIT	PAPER NUMBER
1635	

DATE MAILED: 09/22/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)
	09/895,435	STEWART ET AL.
	Examiner	Art Unit
	Sean R McGarry	1635

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *09 June 2004*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-5,11-20 and 53-74* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-5,11-20,53-55,57-60,62-65 and 67-74* is/are rejected.

7)☒ Claim(s) *56,61 and 66* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *sequence alignment*.

DETAILED ACTION

Claims 1-5, 11-20, 53-55, 57-60, 62-65, and 67-74 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The amendment filed 6/8/04 introduces new matter into the disclosure. The added material which is not supported by the original disclosure is as follows: The language introduced into the claims refers to functional variants that alter SEQ ID NO: 3 only in the central crossover region and also refers to inverted repeat alterations at this location. Applicant has pointed to page 5 of the specification. It is noted that nowhere one page 5 is there a reference to crossover region modifications or inverse repeat modifications in the context of the claimed invention.

Applicant is required to cancel the new matter in the reply to this Office Action.

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Claims 1-5, 11-13, 15-20, 54, 55, 57, 59, 60, 64, 65, and 67 remain and new claims 68-74 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably

convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. This is a written description rejection.

The specification discloses SEQ ID NO:3 which corresponds to the cDNA/genomic DNA encoding the human/rat/mouse species of TRT promoter and SEQ ID NO: 2 which corresponds to TRT'. SEQ ID NO: 3 and SEQ ID NO: 2 meet the written description provisions of 35 USC 112, first paragraph. However, the claims are directed to encompass "functional variants thereof" which may correspond to sequences from other species, mutated sequences, allelic variants, splice variants, sequences that have a recited degree of identity (similarity, homology), functional variants that are altered from SEQ ID NO: 3 only in the crossover region including, but not limited to inverted repeat, and so forth. None of these sequences meet the written description provision of 35 USC 112, first paragraph. The specification provides insufficient written description to support the genus encompassed by the claim. It is noted that applicant's specification provides a description of what might be a "functional variant" at pages 6 and 11, for example. Applicant description/definition requires only that at least some change in sequence is made. There is no upper limit to the changes and the functional variants read on species with no apparent structural similarity as SEQ ID NO: 2 or 3 but which would have the same function. It is noted that the specification provides a few examples, but only examples where the structure is quite similar to that of SEQ ID NO:2 or 3 for example. The specification provides a method to screen for

functional variants. The specification provides potential methods for finding species of the claimed invention , but fails to provide the structure of these species.

Vas-Cath Inc. v. Mahurkar, 19 USPQ2d 1111, makes clear that "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession *of the invention.* The invention is, for purposes of the 'written description' inquiry, *whatever is now claimed.*" (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See Vas-Cath at page 1116.)

With the exception of SEQ ID NO: 3 or 2, the skilled artisan cannot envision the detailed chemical structure of the encompassed polynucleotides, **regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method for isolating it. The nucleic acid itself is required.** See Fiers v. Revel, 25 USPQ2d 1601, 1606 (CAFC 1993) and Amgen Inc. V. Chugai Pharmaceutical Co. Ltd., 18 USPQ2d 1016. In Fiddes v. Baird, 30 USPQ2d 1481, 1483, claims directed to mammalian FGF's were found unpatentable due to lack of written description for the broad class. The specification provided only the bovine sequence.

Finally, University of California v. Eli Lilly and Co., 43 USPQ2d 1398, 1404, 1405 held that:

> ...To fulfill the written description requirement, a patent specification must describe an invention and do so in sufficient detail that one skilled in the art can

clearly conclude that "the inventor invented the claimed invention." *Lockwood v. American Airlines, Inc.* , 107 F.3d 1565, 1572, 41 USPQ2d 1961, 1966 (1997); In *re Gosteli* , 872 F.2d 1008, 1012, 10 USPQ2d 1614, 1618 (Fed. Cir. 1989) (" [T]he description must clearly allow persons of ordinary skill in the art to recognize that [the inventor] invented what is claimed."). Thus, an applicant complies with the written description requirement "by describing the invention, with all its claimed limitations, not that which makes it obvious," and by using "such descriptive means as words, structures, figures, diagrams, formulas, etc., that set forth the claimed invention." *Lockwood*, 107 F.3d at 1572, 41 USPQ2d at 1966.

An adequate written description of a DNA, such as the cDNA of the recombinant plasmids and microorganisms of the '525 patent, "requires a precise definition, such as by structure, formula, chemical name, or physical properties," not a mere wish or plan for obtaining the claimed chemical invention. *Fiers v. Revel* , 984 F.2d 1164, 1171, 25 USPQ2d 1601, 1606 (Fed. Cir. 1993). Accordingly, "an adequate written description of a DNA requires more than a mere statement that it is part of the invention and reference to a potential method for isolating it; what is required is a description of the DNA itself." Id. at 1170, 25 USPQ2d at 1606.

The name cDNA is not itself a written description of that DNA; it conveys no distinguishing information concerning its identity. While the example provides a

process for obtaining human insulin-encoding cDNA, there is no further information in the patent pertaining to that cDNA's relevant structural or physical characteristics; in other words, it thus does not describe human insulin cDNA. Describing a method of preparing a cDNA or even describing the protein that the cDNA encodes, as the example does, does not necessarily describe the cDNA itself. No sequence information indicating which nucleotides constitute human cDNA appears in the patent, as appears for rat cDNA in Example 5 of the patent. Accordingly, the specification does not provide a written description of the invention of claim 5.

Therefore, only SEQ ID NO: 3 or 2 but not the full breadth of the claim (or none of the sequences encompassed by the claim) meets the written description provision of 35 USC 112, first paragraph. The species specifically disclosed are not representative of the genus because the genus is highly variant. Applicant is reminded that Vas-Cath makes clear that the written description provision of 35 USC 112 is severable from its enablement provision. (See page 1115.)

Applicants arguments filed 6/08/04 have been considered but are not persuasive.

Applicant argues that the invention is now limited to functional variants where the variants differ from SEQ ID NO: 3 only in the crossover region. Applicant asserts that such functional variants are within the scope of the invention and that such variants are sufficiently described at page 5 of the specification. It is noted that there is no disclosure of a central crossover region in the context of the claimed invention on page 5. There

are no functional variants disclosed that posses the requisite function of the exemplified nucleic acids. The declaration of Bernard Hallet does not take the place of an adequate description of the invention in the specification. It is again noted that **regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method for isolating it. The nucleic acid itself is required**. See Fiers v. Revel, 25 USPQ2d 1601, 1606 (CAFC 1993). Applicant is reminded that Vas-Cath makes clear that the written description provision of 35 USC 112 is severable from its enablement provision. (See page 1115.) So, although the declaration might provide evidence of enablement for a particular embodiment, it does not remedy the lack of an adequate written description of the invention.

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1-3, 11-13, 53, 55, 58, 60 remain rejected under 35 U.S.C. 102(b) as being anticipated by Mahillon et al [NAR Vol. 16(24):1988].

Mahillon et al disclose a pGI2 plasmid sequence (a vector with sequences other than Tn4430 (ie "heterologous" as defined in the instant specification at page 6, for example)). The sequence includes SEQ ID NO:3 and SEQ ID NO:2 and does not

contain more than 200 contiguous nucleotides of SEQ ID NO: 4. The pGI2 plasmid was cloned and characterized in E.coli cells.

Claims 1-3, 11-13, 53, 55, 58, and 60 remain under 35 U.S.C. 102(b) as being anticipated by Mahillon et al [The EMBO Journal Vol. 7(5):1515-1526, 1988].

Mahillon et al have disclosed several plasmid vectors that comprises SEQ ID NO: 3 and SEQ ID NO: 2 while not comprising more 100 contiguous nucleotides of SEQ ID NO: 4. Mahillon et al have disclosed that the plasmid vectors have various selectable markers which of themselves would be "heterologous" nucleic acid sequences as defined in the instant specification (see page 6, for example).

Claims 20, 63, and 65 remain rejected under 35 U.S.C. 102(b) as anticipated by or, in the alternative, under 35 U.S.C. 103(a) as obvious over Mahillon et al [The EMBO Journal Vol. 7(5):1515-1526, 1988].

Mahillon et al is relied upon as above. Additionally Mahillon et al disclose that the vectors described encode TnpI and further the plasmids are in E. coli cells which are capable of expressing such heterologous proteins from vectors. Although not specifically disclosed in the reference it would appear inherent in the reference that the disclosed compositions/compounds in [a] container/s since one would keep such compositions in a container to keep the experimental compounds free from contamination, to minimize loss due to evaporation, or to keep them [the experimental

compounds] from covering a work area, for example. If the compositions/compounds disclosed in the reference were not in containers it would have been obvious to do so for the same reasons above where inherency has been presumed.

Applicants arguments filed 6/08/04 have been considered but are not persuasive.

Applicant argues that the prior art contains all 249 nucleotides of SEQ ID NO: 4 and provides sequences as evidence. These sequences are not convincing since these sequences are not those sequences of the prior art applicant is provided as an attachment to this Official Action an alignment of the prior art reference and SEQ ID NO: 4 of the instant application. It is clear that neither sequence contains more than 200 contiguous nucleates of SEQ ID NO: 4. Applicant argues that one would not provide the possible constituents of the claimed kits in separate containers. It is noted that the rejection of record clearly set forth the reasons for storage in a container or containers. Applicant argues as if the only other possible constituent is a TnpI protein. This is not the case since the invention also considers a cell capable of expressing a TnpI protein, for example.

Claims 56, 61, and 66 are objected to as being dependent upon a rejected base claim, but would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims.

Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Sean R McGarry whose telephone number is (571) 272-0761. The examiner can normally be reached on M-Th (6:00-4:30).

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, John LeGuyader can be reached on (571) 272-0760. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Sean R McGarry
Primary Examiner
Art Unit 1635

1635

SRM

ATTACHMENT B OFFICE ACTION

NOT SEARCH NOTES

ATTACHMENT (PLEASE SCAN - NOT SEARCH NOTES)

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 28, 2004, 05:52:06 ; Search time 1253.82 Seconds
(without alignments)
8607.626 Million cell updates/sec

SEQ ID NO: 4

Title: US-09-895-435A-4
Perfect score: 249
Sequence: 1 ggggtaccgccagcatttcg.....gacgcggaggaaatcacatg 249

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	249	100.0	249	6	AX671525	AX671525 Sequence
2	244	98.0	244	6	AX671522	AX671522 Sequence
3	241	96.8	4149	1	BTTN4430	X07651 Bacillus th
4	241	96.8	9672	1	BTPGI2XX	X13481 Bacillus th
5	118	47.4	118	6	AX671523	AX671523 Sequence
6	114.4	45.9	116	6	AX671528	AX671528 Sequence
7	114.4	45.9	116	6	AX671529	AX671529 Sequence
8	64	25.7	116	6	AX671530	AX671530 Sequence
9	53	21.3	2015	3	AB064263	AB064263 Plasmodiu
c 10	53	21.3	158548	3	PFMAL3P2	AL034558 Plasmodiu
c 11	53	21.3	205429	2	AC005506	AC005506 Plasmodiu
12	53	21.3	253132	3	AE014846	AE014846 Plasmodiu
13	52.8	21.2	609	8	PRU251061	AJ251061 Plagiocha
14	52	20.9	1018	8	AF402569	AF402569 Clavija s
c 15	51.8	20.8	29150	3	AC115683	AC115683 Dictyoste
16	51.8	20.8	83332	9	AC095051	AC095051 Homo sapi
17	51.8	20.8	343050	3	PFA929353	AL929353 Plasmodiu
18	51.4	20.6	271546	3	AE014843	AE014843 Plasmodiu
c 19	51.2	20.6	61869	2	AC104381	AC104381 Homo sapi
20	51	20.5	124	6	AX671531	AX671531 Sequence
21	51	20.5	60529	2	AC144825	AC144825 Danio rer
c 22	51	20.5	90859	8	AC005561	AC005561 Arabidops
c 23	51	20.5	252632	3	AE014818	AE014818 Plasmodiu
c 24	50.8	20.4	203958	5	AL954339	AL954339 Zebrafish
c 25	50.4	20.2	110000	2	PFMAL13_22	Continuation (23 o
c 26	50.2	20.2	6550	6	AX344862	AX344862 Sequence
27	50.2	20.2	99858	9	HSJ1059A9	AL118524 Human DNA
c 28	50.2	20.2	103942	2	AC091859	AC091859 Homo sapi
29	50.2	20.2	110000	2	AC117408_1	Continuation (2 of
30	50.2	20.2	113372	9	AL161613	AL161613 Human DNA
31	50.2	20.2	148263	9	AC091988	AC091988 Homo sapi
c 32	50.2	20.2	172043	9	AC026797	AC026797 Homo sapi
33	50.2	20.2	173181	9	BX005037	BX005037 Human DNA
c 34	50.2	20.2	182366	9	AL591926	AL591926 Human DNA
c 35	50.2	20.2	188062	9	AL162731	AL162731 Human DNA
c 36	50.2	20.2	250029	3	AE014820	AE014820 Plasmodiu
c 37	50.2	20.2	250707	3	AE014848	AE014848 Plasmodiu
c 38	50.2	20.2	340552	3	PFA929354	AL929354 Plasmodiu
c 39	50	20.1	11308	1	AE007654	AE007654 Clostridi
40	50	20.1	163316	9	AL161420	AL161420 Human DNA
c 41	50	20.1	182083	2	BX539308	BX539308 Danio rer
c 42	49.8	20.0	32392	6	AX392737	AX392737 Sequence
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c 45	49.8	20.0	232392	14	AF250284	AF250284 Amsacta m

ALIGNMENTS

RESULT 1
AX671525
LOCUS AX671525 249 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 4 from Patent WO03004652.
ACCESSION AX671525
VERSION AX671525.1 GI:29329875
KEYWORDS .
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1
AUTHORS Stewart,F.A., Zhang,Y. and Hallet,B.
TITLE Use of a tyrosine recombinase for genetic engineering
JOURNAL Patent: WO 03004652-A 4 16-JAN-2003;

```
            The European Molecular Biology Laboratory (DE) ; L'Universite
            Catholique De louvain (BE)
FEATURES             Location/Qualifiers
     source          1. .249
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.2e-32;
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Qy          1 GGGGTACCGCCAGCATTTCGGAAAAAAACCACGCTAAGAAAATCAGAGTTAAAAAATCAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGTACCGCCAGCATTTCGGAAAAAAACCACGCTAAGAAAATCAGAGTTAAAAAATCAG 60

Qy         61 AAAATATATCATTATTCCTTGACACATACATGTTCTTTTTTTTATACAAAAAATAATACAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 CACAATATTAATTGTGTTGTATTAGGTGTTATAATAAATATAAATCTAGGGGTTTAACGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACAATATTAATTGTGTTGTATTAGGTGTTATAATAAATATAAATCTAGGGGTTTAACGC 180

Qy        181 AACACAATTTATCGATAAATAAATACTTTTAGACGCAACACAATTTATAGACGCGGAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACACAATTTATCGATAAATAAATACTTTTAGACGCAACACAATTTATAGACGCGGAGGA 240

Qy        241 AATCACATG 249
              |||||||||
Db        241 AATCACATG 249


RESULT 2
AX671522
LOCUS       AX671522                 244 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 1 from Patent WO03004652.
ACCESSION   AX671522
VERSION     AX671522.1  GI:29329872
KEYWORDS    .
SOURCE      Bacillus thuringiensis
  ORGANISM  Bacillus thuringiensis
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
            cereus group.
REFERENCE   1
  AUTHORS   Stewart,F.A., Zhang,Y. and Hallet,B.
  TITLE     Use of a tyrosine recombinase for genetic engineering
  JOURNAL   Patent: WO 03004652-A 1 16-JAN-2003;
            The European Molecular Biology Laboratory (DE) ; L'Universite
            Catholique De louvain (BE)
FEATURES             Location/Qualifiers
     source          1. .244
                     /organism="Bacillus thuringiensis"
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 8.3e-32;
  Matches  244;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GGTACCGCCAGCATTTCGGAAAAAAACCACGCTAAGAAAATCAGAGTTAAAAAATCAGAA 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGTACCGCCAGCATTTCGGAAAAAAACCACGCTAAGAAAATCAGAGTTAAAAAATCAGAA 60

Qy         63 AATATATCATTATTCCTTGACACATACATGTTCTTTTTTTTATACAAAAAATAATACAACA 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATATATCATTATTCCTTGACACATACATGTTCTTTTTTTTATACAAAAAATAATACAACA 120

Qy        123 CAATATTAATTGTGTTGTATTAGGTGTTATAATAAATATAAATCTAGGGGTTTAACGCAA 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAATATTAATTGTGTTGTATTAGGTGTTATAATAAATATAAATCTAGGGGTTTAACGCAA 180
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Qy        183 CACAATTTATCGATAAATAAATACTTTTAGACGCAACACAATTTATAGACGCGGAGGAAA 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CACAATTTATCGATAAATAAATACTTTTAGACGCAACACAATTTATAGACGCGGAGGAAA 240

Qy        243 TCAC 246
              ||||
Db        241 TCAC 244


RESULT 3
BTTN4430
LOCUS       BTTN4430                 4149 bp    DNA     linear   BCT 12-SEP-1993
DEFINITION  Bacillus thuringiensis transposon Tn4430.
ACCESSION   X07651
VERSION     X07651.1  GI:40347
KEYWORDS    plasmid; resolvase; tnpA gene; tnpI gene; transposase; transposon.
SOURCE      Bacillus thuringiensis
  ORGANISM  Bacillus thuringiensis
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
            cereus group.
REFERENCE   1  (bases 1 to 4149)
  AUTHORS   Mahillon,J. and Lereclus,D.
  TITLE     Structural and functional analysis of Tn4430: identification of an
            integrase-like protein involved in the co-integrate-resolution
            process
  JOURNAL   EMBO J. 7 (5), 1515-1526 (1988)
  MEDLINE   88312602
   PUBMED   2842151
COMMENT     Data kindly reviewed (03-APR-1989) by Lereclus D.
FEATURES             Location/Qualifiers
     source          1. .4149
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                     /mol_type="genomic DNA"
                     /strain="H1.1"
                     /db_xref="taxon:1428"
                     /map="plasmid pGI2"
                     /clone="pGI200"
                     /clone_lib="pBR322"
     repeat_unit     1. .38
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                     - 284)"
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                     /db_xref="SWISS-PROT:P10020"
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                     TGECIIRSGKGGKQRIVLLNSKVLSAIKDYLIDRKTYSTAHESPYLFISKKREKLDRT
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                     LKNKMELL"
     CDS             1120. .4083
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                     987)"
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                     /transl_table=11
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                     /db_xref="GI:40349"
                     /db_xref="GOA:P10021"
                     /db_xref="SWISS-PROT:P10021"
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                     EHLGEIRTEYGYQNFSSEYKETLLQFLVQQAMDNNNTLYLIEITISTLRKTKVILPAM
                     YVIEDIVWEAKQQADQKVYSILHDGLVQEQKDQLDALLLPTINGKSPLAWLKDVPAQP
                     SPESPLKVIDRLQFVQKIGLTIDTTKINTNRLRQLARLGSKYEPYAFRRFNEVKRYSM
                     LVSFLLEITQDLIDYAIEIHDRLMMNLQTKGKKEQDEIQQANGKKLNEKILQFITVCG
                     TLIEAKETGKDAFAALDEVMSWNEMVESVEEAKQLSRPLNYDYLDLLNTRYSYVRRYA
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     repeat_unit     4112. .4149
                     /note="inverted repeat A'"
ORIGIN

  Query Match            96.8%;  Score 241;  DB 1;  Length 4149;
  Best Local Similarity  98.0%;  Pred. No. 1.4e-31;
  Matches  244;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GGGGTACCGCCAGCATTTCGGAAAAAAACCACGCTAAGAAAATCAGAGTTAAAAAATCAG 60
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Db          1 GGGGTACCGCCAGCATTTCGGAAAAAAACCACGCTAAGAAAATCAGAGTTAAAAAATCAG 60

Qy         61 AAAATATATCATTATTCCTTGACACATACATGTTCTTTTTTTATACAAAAAATAATACAA 120
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Db         61 AAAATATATCATTATTCCAAGACACATACAGTGTCTTTTTTTATACAAAAAATAATACAA 120

Qy        121 CACAATATTAATTGTGTTGTATTAGGTGTTATAATAAATATAAATCTAGGGGTTTAACGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACAATATTAATTGTGTTGTATTAGGTGTTATAATAAATATAAATCTAGGGGTTTAACGC 180

Qy        181 AACACAATTTATCGATAAATAAATACTTTTAGACGCAACACAATTTATAGACGCGGAGGA 240
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Db        181 AACACAATTTATCGATAAATAAATACTTTTAGACGCAACACAATTTATAGACGCGGAGGA 240

Qy        241 AATCACATG 249
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Db        241 AATCACATG 249


RESULT 4
BTPGI2XX
LOCUS       BTPGI2XX                9672 bp    DNA     linear   BCT 07-JUL-2002
DEFINITION  Bacillus thuringiensis plasmid pGI2 with transposon Tn4430.
ACCESSION   X13481
VERSION     X13481.1  GI:3171732
KEYWORDS    plasmid; plasmid pGI2; recombinase; resolvase; transposase;
            transposon; unidentified reading frame.
SOURCE      Bacillus thuringiensis
  ORGANISM  Bacillus thuringiensis
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
            cereus group.
REFERENCE   1  (bases 1 to 6999)
  AUTHORS   Mahillon,J. and Seurinck,J.
  TITLE     Complete nucleotide sequence of pGI2, a Bacillus thuringiensis
            plasmid containing Tn4430
  JOURNAL   Nucleic Acids Res. 16 (24), 11827-11828 (1988)
  MEDLINE   89098342
   PUBMED   3211758
REFERENCE   2
  AUTHORS   Mahillon,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-NOV-1988) Mahillon J., Plant Genetics Systems, J
            Plateaustraat 22, B-9000 Gent, Belgium
  REMARK    revised by [3]
REFERENCE   3  (bases 1 to 9672)
  AUTHORS   Hoflack,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAR-1998) Hoflack L., Plant Genetics Systems, J
            Plateaustraat 22, B-9000 Gent, Belgium
COMMENT     On Jun 2, 1998 this sequence version replaced gi:40316.
FEATURES             Location/Qualifiers
     source          1..9672
                     /organism="Bacillus thuringiensis"
                     /mol_type="genomic DNA"
                     /strain="thuringiensis H1.1."
                     /db_xref="taxon:1428"
                     /plasmid="pGI2"
repeat_region        493. .4651
                     /transposon="Tn4430"
repeat_region        493. .497
                     /note="direct repeat 1"
repeat_unit          498. .535
                     /note="inverted repeat A"
CDS                  744. .1598
                     /codon_start=1
                     /transl_table=11
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                     /protein_id="CAA31832.1"
                     /db_xref="GI:40317"
                     /db_xref="GOA:P10020"
                     /db_xref="SWISS-PROT:P10020"
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                     VVNRIFKSYSNVITPHQLRHFFCTNAIEKGFSIHEVANQAGHSNIHTTLLYTNPNQLQ
                     LKNKMELL"
CDS                  1617. .4580
                     /codon_start=1
                     /transl_table=11
                     /product="TnpA transposase"
                     /protein_id="CAA31833.1"
                     /db_xref="GI:40318"
                     /db_xref="GOA:P10021"
                     /db_xref="SWISS-PROT:P10021"
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                     EHLGEIRTEYGYQNFSSEYKETLLQFLVQQAMDNNNTLYLIEITISTLRKTKVILPAM
                     YVIEDIVWEAKQQADQKVYSILHDGLVQEQKDQLDALLLPTINGKSPLAWLKDVPAQP
                     SPESFLKVIDRLQFVQKIGLTIDTTKINTNRLRQLARLGSKYEPYAFRRFNEVKRYSM
                     LVSFLLEITQDLIDYAIEIHDRLMMNLQTKGKKEQDEIQQANGKKLNEKILQFITVCG
                     TLIEAKETGKDAFAALDEVMSWNEMVESVEEAKQLSRPLNYDYLDLLNTRYSYVRRYA
                     PTLLRSLHFRATKSGEPVLQALDTIHELNETGKRKVPHGAPLHFVSNRWQKHVYDDDG
                     NINRHYYELAALTELRNHIRSGDIFVSGSRHHKAFDDYLIPYDEWNEVSNIPNGLTAP
                     LKAEDYITDRINRLNEHLEWLSKNSZKLEGVDISQGKLHVERLDRGTPEEAKAFSKLL
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                     LSIAVRSLHADSNPHYGTGKGGTIYRFVSDQLSAYHVKVITTNARDALHVLDGLLHHE
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                     KGKINVKLIKENYEDIRRLAYSVQTGKVSSALIMGKLGSYARQNKLATALGEMGRIEK
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repeat_unit          4609. .4646
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repeat_region        4647. .4651
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CDS                  4859. .5473
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                     /db_xref="SWISS-PROT:P10022"
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CDS                  6037. .6849
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                     NWMQKYTASGKWIKVYRLKDQTLARDVARYADRNFYSTTGSATKNVYLDYGIDTHLYQ
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                     IEMKKLKYPPLQ"
     CDS             7829. .9166
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                     /db_xref="GI:40322"
                     /db_xref="GOA:P10025"
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ORIGIN

  Query Match          96.8%;  Score 241;  DB 1;  Length 9672;
  Best Local Similarity  98.0%;  Pred. No. 1.2e-31;
  Matches  244;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GGGGTACCGCCAGCATTTCGGAAAAAAACCACGCTAAGAAAATCAGAGTTAAAAAATCAG 60
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Db        498 GGGGTACCGCCAGCATTTCGGAAAAAAACCACGCTAAGAAAATCAGAGTTAAAAAATCAG 557

Qy         61 AAAATATATCATTATTCCTTGACACATACATGTTCTTTTTTTATACAAAAAATAATACAA 120
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Db        558 AAAATATATCATTATTCCAAGACACATACAGTGTCTTTTTTTATACAAAAAATAATACAA 617

Qy        121 CACAATATTAATTGTGTTGTATTAGGTGTTATAATAAATATAAATCTAGGGGTTTAACGC 180
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Db        618 CACAATATTAATTGTGTTGTATTAGGTGTTATAATAAATATAAATCTAGGGGTTTAACGC 677

Qy        181 AACACAATTTATCGATAAATAAATACTTTTAGACGCAACACAATTTATAGACGCGGAGGA 240
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Db        678 AACACAATTTATCGATAAATAAATACTTTTAGACGCAACACAATTTATAGACGCGGAGGA 737

Qy        241 AATCACATG 249
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Db        738 AATCACATG 746


RESULT 5
AX671523
LOCUS       AX671523                118 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 2 from Patent WO03004652.
ACCESSION   AX671523
VERSION     AX671523.1  GI:29329873
KEYWORDS    .
SOURCE      Bacillus thuringiensis
  ORGANISM  Bacillus thuringiensis
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
            cereus group.
REFERENCE   1
  AUTHORS   Stewart,F.A., Zhang,Y. and Hallet,B.
  TITLE     Use of a tyrosine recombinase for genetic engineering
  JOURNAL   Patent: WO 03004652-A 2 16-JAN-2003;
            The European Molecular Biology Laboratory (DE) ; L'Universite
            Catholique De louvain (BE)
FEATURES             Location/Qualifiers
     source          1. .118
                     /organism="Bacillus thuringiensis"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1428"
ORIGIN

  Query Match          47.4%;  Score 118;  DB 6;  Length 118;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-10;
  Matches  118;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        113 TAATACAACACAATATTAATTGTGTTGTATTAGGTGTTATAATAAATATAAATCTAGGGG 172
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Db          1 TAATACAACACAATATTAATTGTGTTGTATTAGGTGTTATAATAAATATAAATCTAGGGG 60

Qy        173 TTTAACGCAACACAATTTATCGATAAATAAATACTTTTAGACGCAACACAATTTATAG 230
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Db         61 TTTAACGCAACACAATTTATCGATAAATAAATACTTTTAGACGCAACACAATTTATAG 118


RESULT 6
AX671528
LOCUS       AX671528                116 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 7 from Patent WO03004652.
ACCESSION   AX671528
VERSION     AX671528.1  GI:29329878
KEYWORDS    .
SOURCE      Bacillus thuringiensis
  ORGANISM  Bacillus thuringiensis
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
            cereus group.
REFERENCE   1
  AUTHORS   Stewart,F.A., Zhang,Y. and Hallet,B.
  TITLE     Use of a tyrosine recombinase for genetic engineering
  JOURNAL   Patent: WO 03004652-A 7 16-JAN-2003;
            The European Molecular Biology Laboratory (DE) ; L'Universite
            Catholique De louvain (BE)
FEATURES             Location/Qualifiers
     source          1. .116
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1428"
ORIGIN

  Query Match          45.9%;  Score 114.4;  DB 6;  Length 116;
  Best Local Similarity  99.1%;  Pred. No. 5.8e-10;
  Matches  115;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        113 TAATACAACACAATATTAATTGTGTTGTATTAGGTGTTATAATAAATATAAATCTAGGGG 172
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Db          1 TAATACAACACAATATTAATTGTGTTGTATTAGGTGTTATAATAAATATATATCTAGGGG 60

Qy        173 TTTAACGCAACACAATTTATCGATAAATAAATACTTTTAGACGCAACACAATTTAT 228
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Db         61 TTTAACGCAACACAATTTATCGATAAATAAATACTTTTAGACGCAACACAATTTAT 116


RESULT 7
AX671529
LOCUS       AX671529                116 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 8 from Patent WO03004652.
ACCESSION   AX671529
VERSION     AX671529.1  GI:29329879
KEYWORDS    .
SOURCE      Bacillus thuringiensis
  ORGANISM  Bacillus thuringiensis
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
            cereus group.
REFERENCE   1
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